> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                        SEQUENCE LISTING
 2
 3    (1)     General Information:
 4
 5          (i) APPLICANT: Gregory, Richard J.
 6                         Wills, Ken N.
 7                         Maneval, Daniel C.
 8
 9         (ii) TITLE OF INVENTION: Recombinant Adenoviral Vector and
10               Methods of Use
11
12        (iii) NUMBER OF SEQUENCES: 9
13
14         (iv) CORRESPONDENCE ADDRESS:
15               (A) ADDRESSEE: Campbell and Flores
16               (B) STREET: 4370 La Jolla Village Drive, Suite 700
17               (C) CITY: San Diego
18               (D) STATE: California
19               (E) COUNTRY: USA
20               (F) ZIP: 92122
21
22          (v) COMPUTER READABLE FORM:
23               (A) MEDIUM TYPE: Floppy disk
24               (B) COMPUTER: IBM PC compatible
25               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26               (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27
28         (vi) CURRENT APPLICATION DATA:
29               (A) APPLICATION NUMBER: US 08/328,673
30               (B) FILING DATE: 25-OCT-1994
31               (C) CLASSIFICATION:
32
33        (vii) PRIOR APPLICATION DATA:
34               (A) APPLICATION NUMBER: US 08/233,777
35               (B) FILING DATE: 19-MAY-1994
36
37        (vii) PRIOR APPLICATION DATA:
38               (A) APPLICATION NUMBER: US 08/142,669
39               (B) FILING DATE: 25-OCT-1993
40
41       (viii) ATTORNEY/AGENT INFORMATION:
42               (A) NAME: Campbell, Cathryn A.
43               (B) REGISTRATION NUMBER: 31,815
44               (C) REFERENCE/DOCKET NUMBER: P-CJ 1192
45
46         (ix) TELECOMMUNICATION INFORMATION:
```

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INPUT SET: S2778.raw

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47              (A) TELEPHONE: (619) 535-9001
48              (B) TELEFAX: (619) 535-8949
49
50
51   (2) INFORMATION FOR SEQ ID NO:1:
52
53        (i) SEQUENCE CHARACTERISTICS:
54              (A) LENGTH: 25 base pairs
55              (B) TYPE: nucleic acid
56              (C) STRANDEDNESS: single
57              (D) TOPOLOGY: linear
58
59
60
61        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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63   CGCCACCGAG GGACCTGAGC GAGTC                                          25
64
65   (2) INFORMATION FOR SEQ ID NO:2:
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67        (i) SEQUENCE CHARACTERISTICS:
68              (A) LENGTH: 20 base pairs
69              (B) TYPE: nucleic acid
70              (C) STRANDEDNESS: single
71              (D) TOPOLOGY: linear
72
73
74
75        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
76
77   TTCTGGGAAG GGACAGAAGA                                               20
78
79   (2) INFORMATION FOR SEQ ID NO:3:
80
81        (i) SEQUENCE CHARACTERISTICS:
82              (A) LENGTH: 25 base pairs
83              (B) TYPE: nucleic acid
84              (C) STRANDEDNESS: single
85              (D) TOPOLOGY: linear
86
87
88
89        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
90
91   CGCGCTAGCT CTGCCCCAAA GAGCT                                          25
92
93   (2) INFORMATION FOR SEQ ID NO:4:
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95        (i) SEQUENCE CHARACTERISTICS:
96              (A) LENGTH: 39 base pairs
97              (B) TYPE: nucleic acid
98              (C) STRANDEDNESS: single
99              (D) TOPOLOGY: linear
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INPUT SET: S2778.raw

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101
102
103        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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105   CGCGGTACCC TCGAGTCTAG ATATTGCCAG TGGTGGAAG                    39
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107   (2) INFORMATION FOR SEQ ID NO:5:
108
109        (i) SEQUENCE CHARACTERISTICS:
110            (A) LENGTH: 35 base pairs
111            (B) TYPE: nucleic acid
112            (C) STRANDEDNESS: single
113            (D) TOPOLOGY: linear
114
115
116
117        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
118
119   CGTGCGGCCG CTGGAGGACT TTGAGGATGT CTGTC                       35
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121   (2) INFORMATION FOR SEQ ID NO:6:
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123        (i) SEQUENCE CHARACTERISTICS:
124            (A) LENGTH: 33 base pairs
125            (B) TYPE: nucleic acid
126            (C) STRANDEDNESS: single
127            (D) TOPOLOGY: linear
128
129
130
131        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
132
133   CGCTCTAGAG AGACCAGTTA GGAAGTTTTC GCA                         33
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135   (2) INFORMATION FOR SEQ ID NO:7:
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137        (i) SEQUENCE CHARACTERISTICS:
138            (A) LENGTH: 2995 base pairs
139            (B) TYPE: nucleic acid
140            (C) STRANDEDNESS: single
141            (D) TOPOLOGY: linear
142
143
144        (ix) FEATURE:
145            (A) NAME/KEY: CDS
146            (B) LOCATION: 139..2922
147
148
149        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
150
151   TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTTGTAA CGGGAGTCGG GAGAGGACGG    60
152
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/328,673*

INPUT SET: S2778.raw

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153     GGCGTGCCCC GCGTGCGCGC GCGTCGTCCT CCCCGGCGCT CCTCCACAGC TCGCTGGCTC        120
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155     CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC           171
156                          Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
157                           1               5                  10

158
159     ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC          219
160     Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
161              15                  20                  25

162
163     CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT          267
164     Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
165              30                  35                  40

166
167     CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA          315
168     Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
169          45                  50                  55

170
171     TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG          363
172     Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
173     60                  65                  70                  75

174
175     TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT          411
176     Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
177                      80                  85                  90

178
179     ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA          459
180     Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
181              95                  100                 105

182
183     GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC          507
184     Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
185              110                 115                 120

186
187     ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT          555
188     Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
189          125                 130                 135

190
191     ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT          603
192     Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
193     140                 145                 150                 155

194
195     GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT          651
196     Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
197                      160                 165                 170

198
199     ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT          699
200     Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser
201                      175                 180                 185

202
203     GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG          747
204     Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
205              190                 195                 200
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INPUT SET: S2778.raw

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206
207   GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG       795
208   Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met
209       205             210                 215
210
211   CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC       843
212   Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
213   220             225                 230                 235
214
215   AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA       891
216   Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg
217               240                 245                 250
218
219   ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA       939
220   Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu
221               255                 260                 265
222
223   GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT       987
224   Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys
225           270                 275                 280
226
227   AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT      1035
228   Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe
229       285                 290                 295
230
231   ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA      1083
232   Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu
233   300                 305                 310                 315
234
235   AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA      1131
236   Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu
237               320                 325                 330
238
239   GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT      1179
240   Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser
241               335                 340                 345
242
243   ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT      1227
244   Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp
245           350                 355                 360
246
247   GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG      1275
248   Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met
249       365                 370                 375
250
251   AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA      1323
252   Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln
253   380                 385                 390                 395
254
255   CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA      1371
256   Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro
257               400                 405                 410
258
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